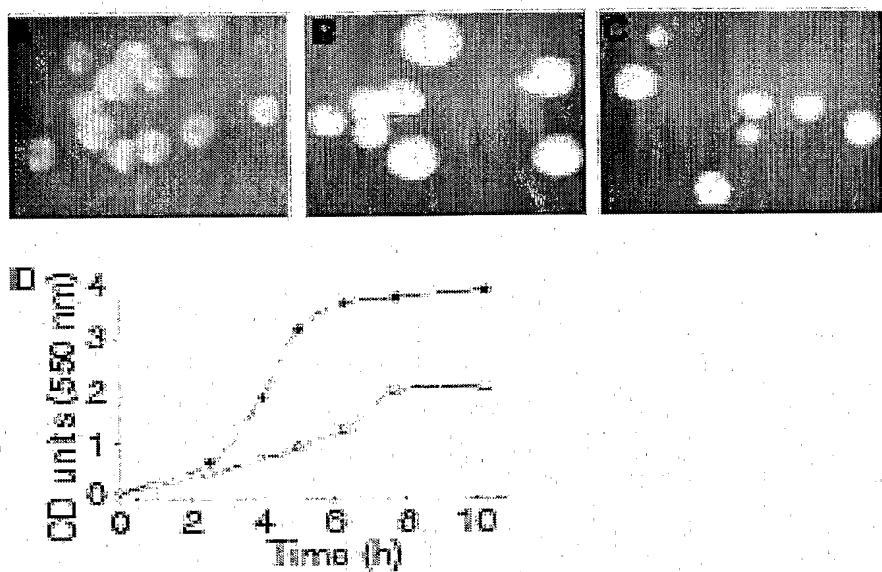Figure 1

Figure 2

Figure 3

Figure 4

Figure 5

extracelullar space

Cys
Cys

outer membrane

periplasm

Cys

Cys
Cys
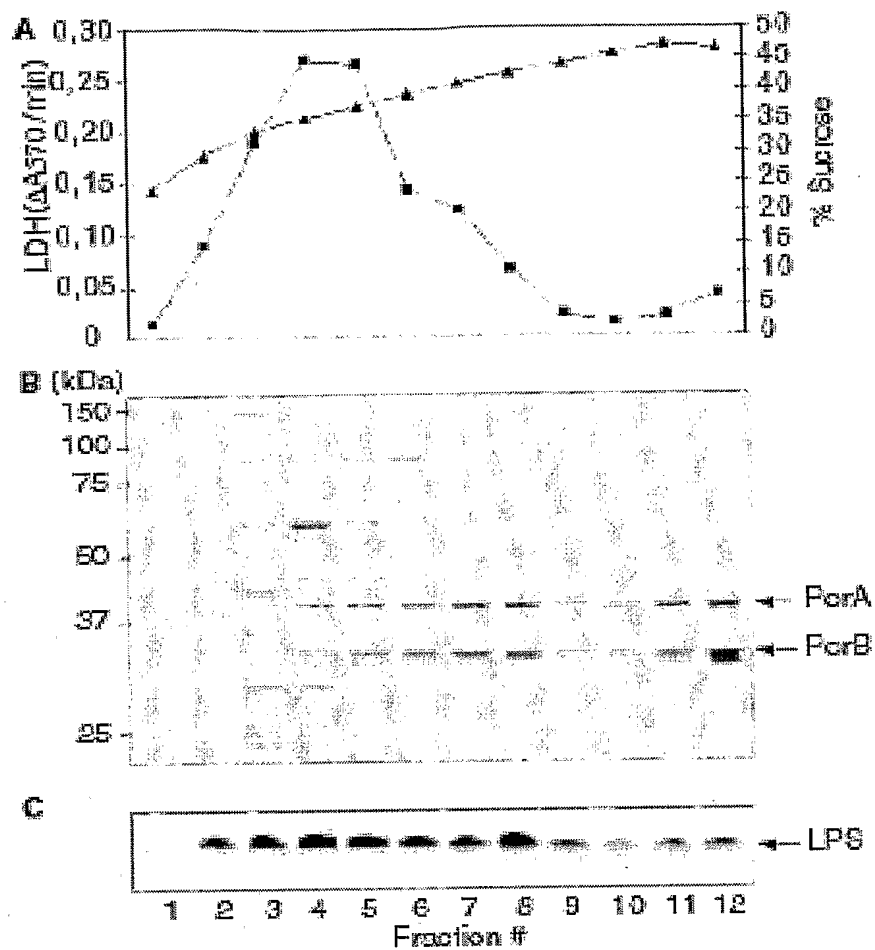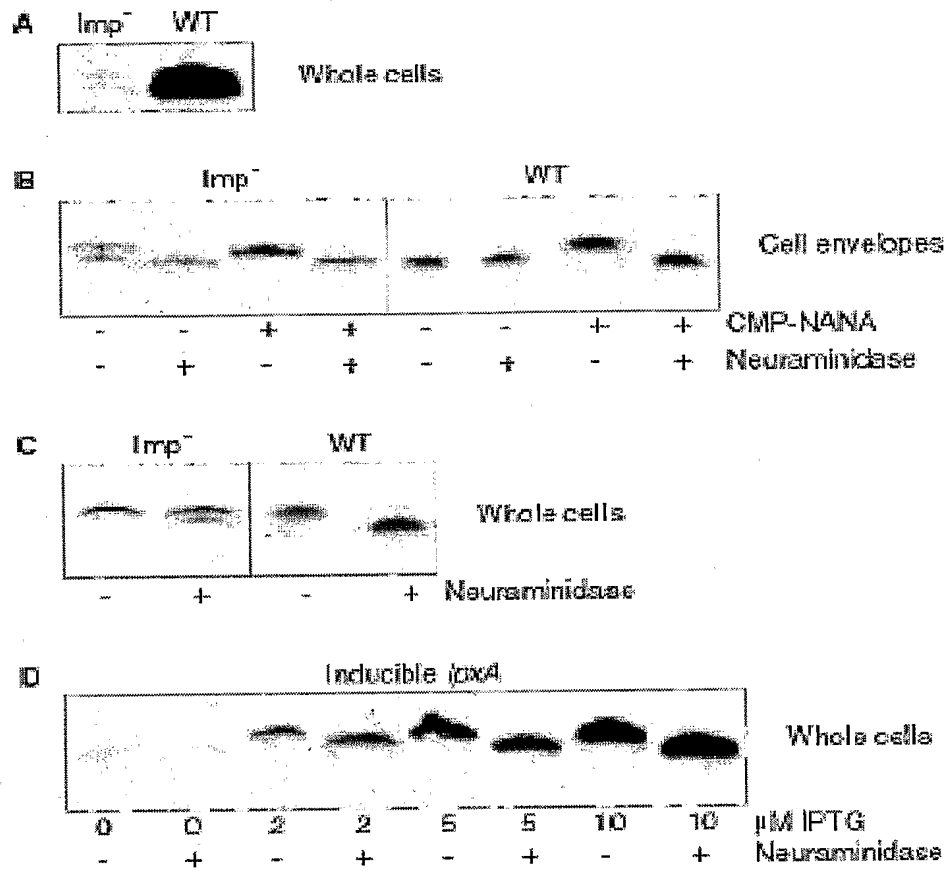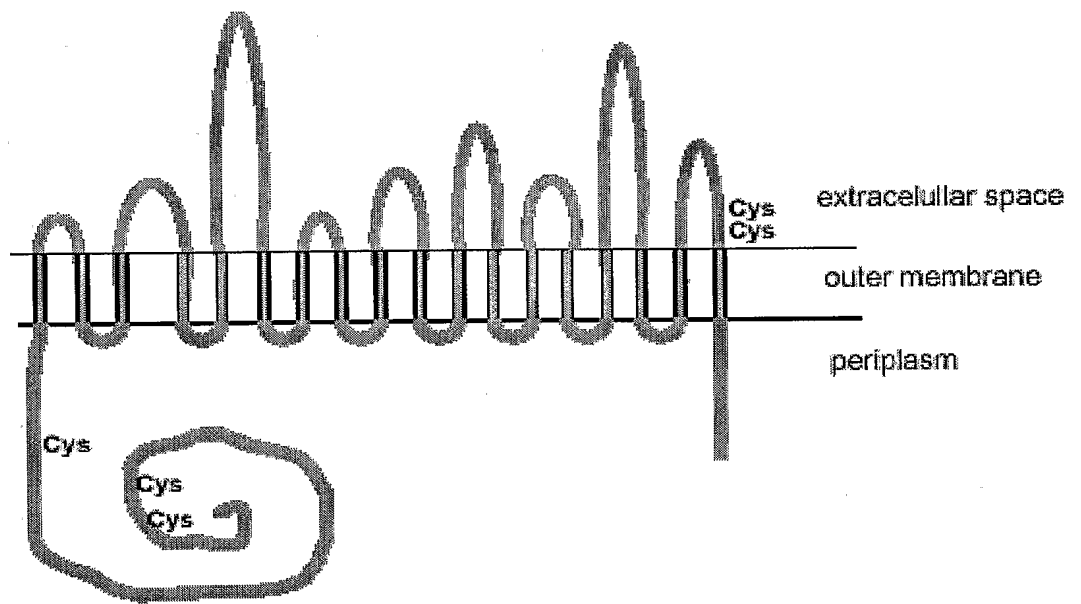
Figure 6

Imp/OstA - SEQ ID No 1
Predicted extracellular loops are indicated in bold

```
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LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL  120
NTDWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMEIEQGGRRLQ  180
SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP  240
IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPSVIGERGAV  300
FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG  360
YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM  420
PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH  480
ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLEPRLFYNYIPAKS  540
QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG  600
QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA  660
SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF  720
EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR  780
MDVAVPGYITAHSLSAGRNKRP  802
```

```
loop 1: 252-271
loop 2: 295-332
loop 3: 357-416
loop 4: 444-455
loop 5: 482-501
loop 6: 537-576
loop 7: 606-624
loop 8: 648-697
loop 9: 721-740
```

Figure 7

```
Imp-FAM18    LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC  60
NMB0280      LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC  60
NMA2207      MARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC  60
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Imp-FAM18    LFCSNESGSPERTEAAVRGSGEASIPEDYTRIVADKVEGQSQVQVRAEGNVVVERNRTTL  120
NMB0280      LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL  120
NMA2207      LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL  120
             *****************:****************::***********************

Imp-FAM18    NTDWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ  180
NMB0280      NTDWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMEIEQGGRRLQ  180
NMA2207      NADWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ  180
             * :*********************************************** *:******

Imp-FAM18    SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP  240
NMB0280      SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP  240
NMA2207      SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP  240
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Imp-FAM18    IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPSVIGERGAV  300
NMB0280      IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPSVIGERGAV  300
NMA2207      IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPGVIGERGAV  300
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Imp-FAM18    FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG  360
NMB0280      FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG  360
NMA2207      FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG  360
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Imp-FAM18    YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM  420
NMB0280      YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM  420
NMA2207      YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM  420
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Imp-FAM18    PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH  480
NMB0280      PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH  480
NMA2207      PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH  480
             ****.:******************************************************

Imp-FAM18    ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGGVLQTLEPRLFYNYIPAKS  540
NMB0280      ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLEPRLFYNYIPAKS  540
NMA2207      ATYYSLNRFGSQEARRVSRTLPIVNIDSGMTFERNTRMFGGGVLQTLEPRLFYNYIPAKS  540
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Imp-FAM18    QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG  600
NMB0280      QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG  600
NMA2207      QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG  600
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Imp-FAM18    QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA  660
NMB0280      QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA  660
NMA2207      QKFYFKNDAVMLDGSVGKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA  660
             ******:************.*********..************************

Imp-FAM18    SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF  720
NMB0280      SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF  720
NMA2207      SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF  720
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Imp-FAM18    EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR  780
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NMA2207      EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR  780
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Imp-FAM18    MDVAVPGYIPAHSLSAGRNKRP  802
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NMA2207      MDVAVPGYIPAHSLSAGRNKRP  802
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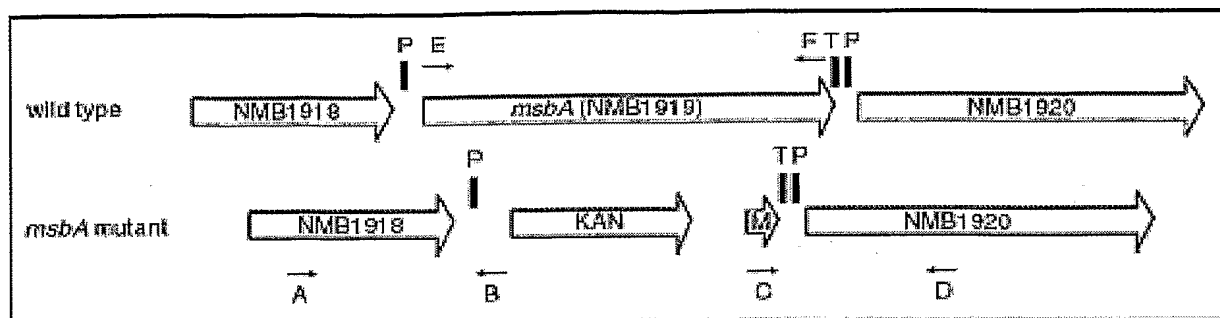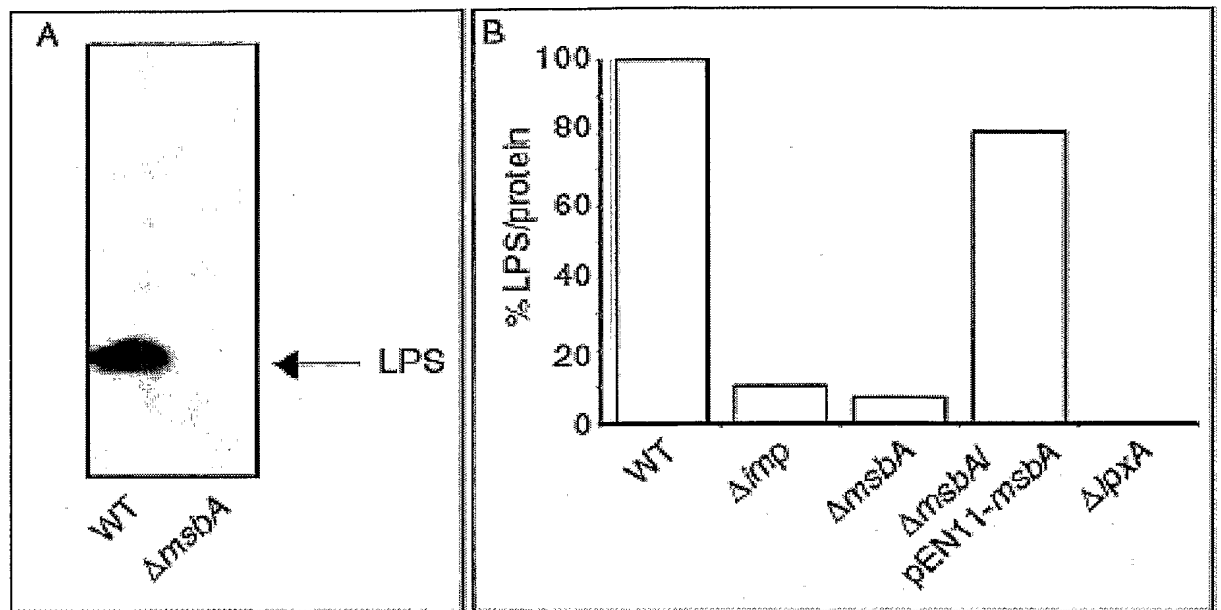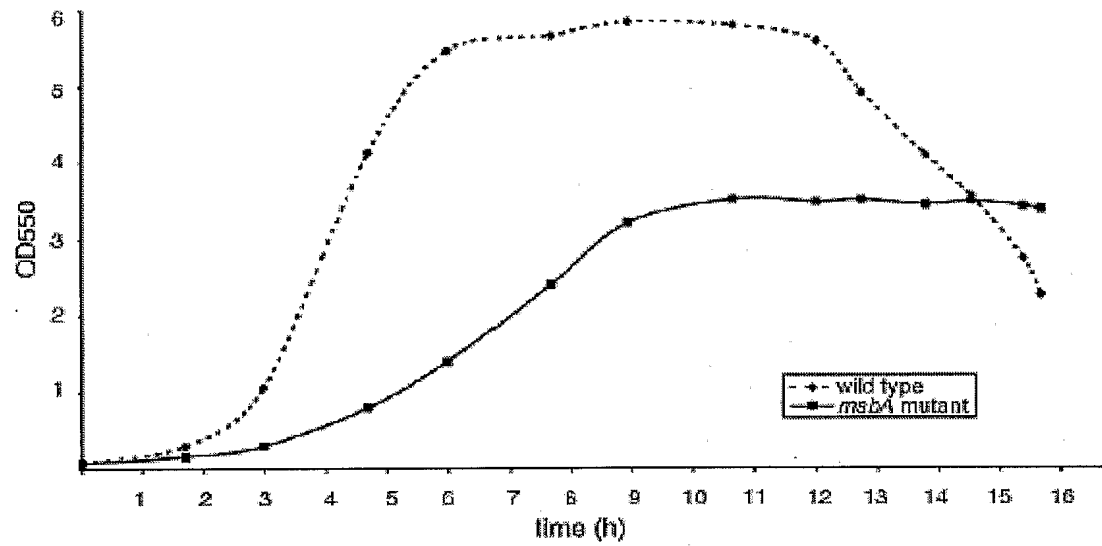
Figure 8

Figure 9

Figure 10

Figure 11
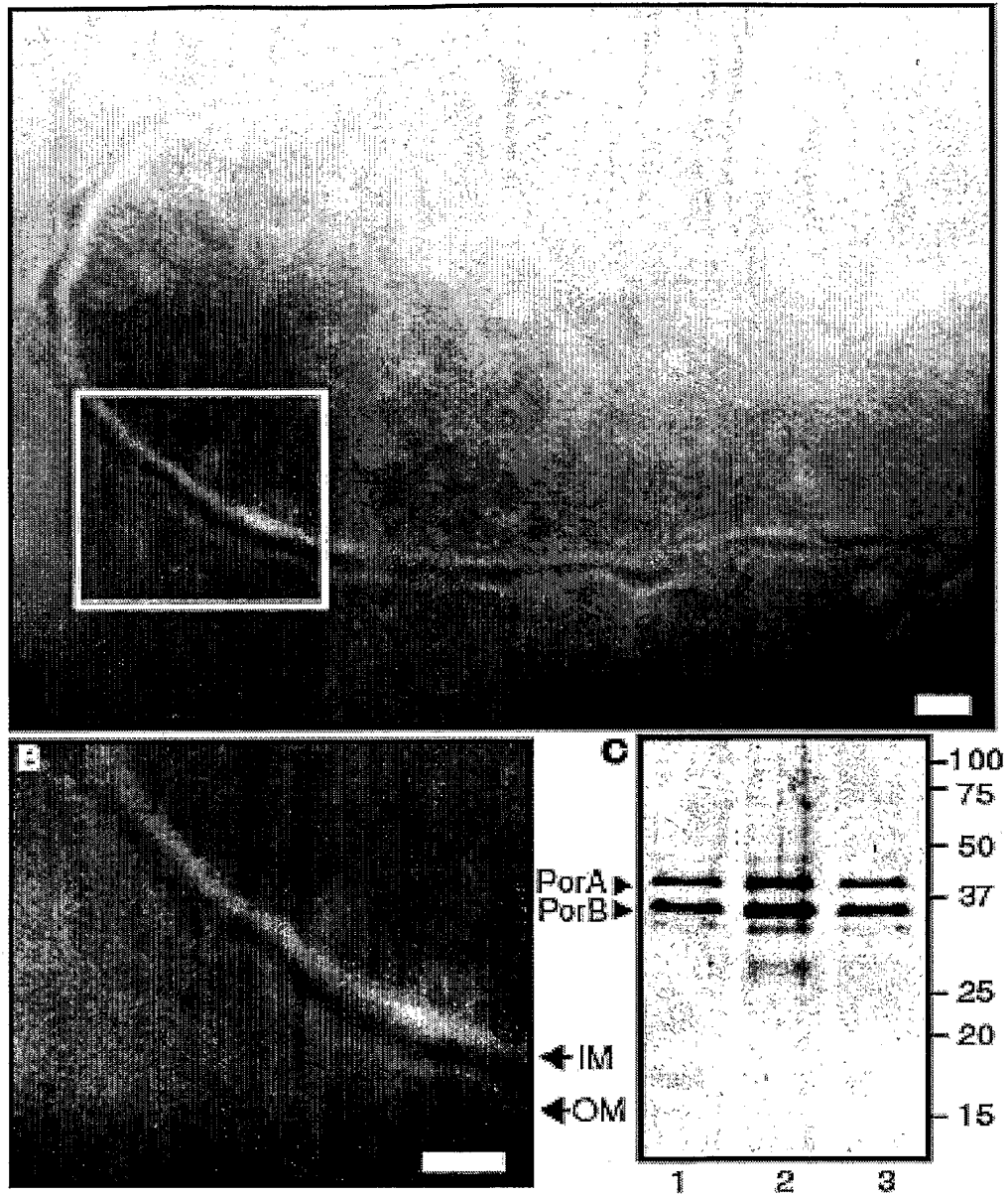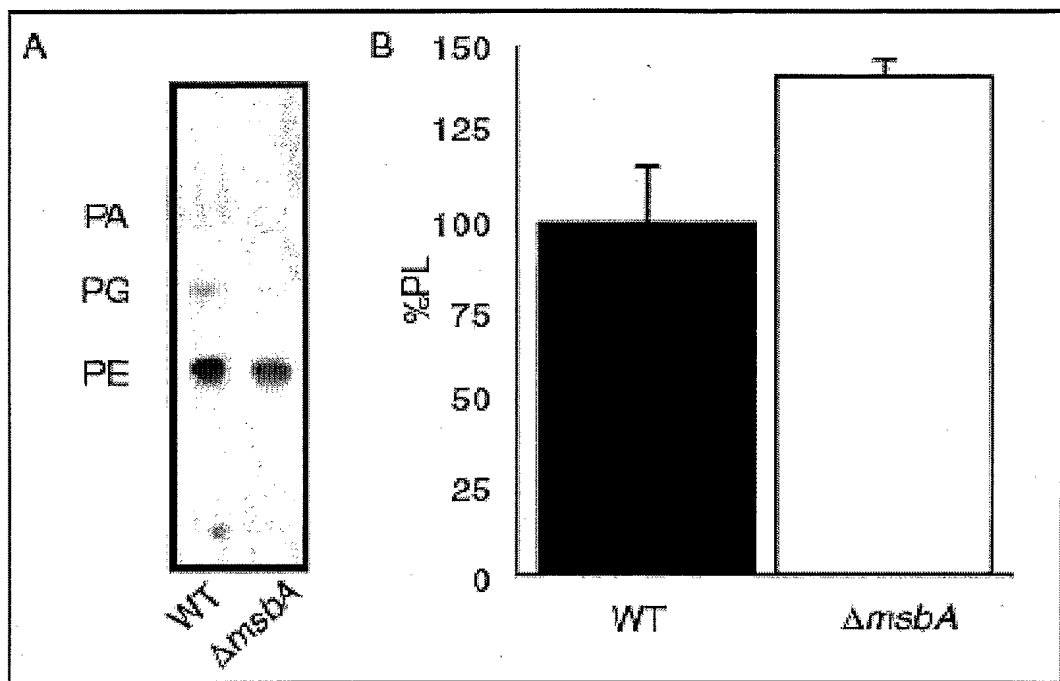
Figure 12

Figure 13

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B

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Figure 14

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Figure 15 A

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Figure 15 B